

BEST AVAILABLE COPY

SEQUENCE LISTING

<100> GENERAL INFORMATION:

<160> NUMBER OF SEQ ID NOS: 48

<200> SEQUENCE CHARACTERISTICS:

<210> SEQ ID NO 1

<211> LENGTH: 33

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence synthetic primer

<400> SEQUENCE: 1

cataaaattt ctaagacgaa ggatccctat gtc 33

<200> SEQUENCE CHARACTERISTICS:

<210> SEQ ID NO 2

<211> LENGTH: 33

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence synthetic primer

<400> SEQUENCE: 2

gagagaaagt tccccgtgtg aattctagct agg 33

<200> SEQUENCE CHARACTERISTICS:

<210> SEQ ID NO 3

<211> LENGTH: 2836

<212> TYPE: DNA

<213> ORGANISM: Ehrlichia risticii

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (175)..(2721)

<400> SEQUENCE: 3

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ttcataacaa aggactatcc tccttgcata aaatttctaa gacgaaaaat ccccl atg 177
Met
1
tca aat gaa aca ctt ttg agc gta ctt tct gal gaa acg cac ttt gct 225
Ser Asn Glu Thr Leu Leu Ser Val Leu Ser Asp Glu Thr His Phe Ala
5 10 15
aat cta gtt gat gaa ctt ctt ctc atc ttg gll aaa gac ugt att ttc 273
Asn Leu Val Asp Glu Leu Leu Leu ile Leu Val Lys Asp Ser Ile Phe
20 25 30
acl caa gta ata aua ggc gag gga aag aca gaa tta aaa gac ata ctt 321
Thr Gln Val Ile Lys Gly Glu Gly Lys Thr Glu Leu Lys Asp Ile Leu
35 40 45
aca gac aac act ggt aag ttt aaa gaa ctt ata guu ugt gca ggt aaa 369
Thr Asp Asn Thr Gly Lys Phe Lys Glu Leu Ile Glu Ser Ala Gly Lys
50 55 60 65
gac ata cta uuu gag ata ctt aca gac aat acc ggc aat ttt aaa gga 417
Asp Ile Leu Lys Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly
70 75 80
ctt ata gaa ggt aat ggt aag acg qag gca aaa gag gta cgc act aat 465
Leu Ile Glu Gly Asn Gly Lys Thr Glu Ala Lys Glu Val Arg Thr Asn

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      85      90      95
gaa aaa ttc aag gag ctt ttt gga agc aat ggt aag gac ata ctg aaa 513
Glu Lys Phe Lys Glu Leu Phe Gly Ser Asn Gly Lys Asp Ile Leu Lys
      100      105      110
gac att ctt act gat aac acc ggt aac ttt aaa ggc cll ata gaa agt 561
Asp Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly Leu Ile Glu Ser
      115      120      125
gca gct aag ggt aag ctg aaa gat ctt ctt att gat gaa aaa ttt caa 609
Ala Ala Lys Gly Lys Leu Lys Asp Leu Leu Ile Asp Glu Lys Phe Gln
      130      135      140      145
aaa tta ttc gag gat gaa acg aaa gct ggt cgt gta aaa gaa ata ctt 657
Lys Leu Phe Glu Asp Glu Thr Lys Ala Gly Arg Val Lys Glu Ile Leu
      150      155      160
aca gac agc aac gct aag gaa atu ctc aca aat gaa gta gca aaa gag 705
Thr Asp Ser Asn Ala Lys Glu Ile Leu Thr Asn Glu Val Ala Lys Glu
      165      170      175
gla cta aau tcc gat aaa ttc aag gaq gca ala act ggc gat ggt aag 753
Val Leu Lys Ser Asp Lys Phe Lys Glu Ala Ile Thr Gly Asp Gly Lys
      180      185      190
gac gca cta aaa gag ata ctt act lgt gat uua ttt aaa gag gct gta 801
Asp Ala Leu Lys Glu Ile Leu Thr Cys Asp Lys Phe Lys Glu Ala Val
      195      200      205
acu ggc aat ggt aaa gac ata cta aaa ggt ata ctt aca gat agc act 849
Thr Gly Asn Gly Lys Asp Ile Leu Lys Gly Ile Leu Thr Asp Ser Thr
      210      215      220      225
ggt aaa ttt aaa gaa ctt ala gaa agt uct agt aaa gac ata cta aaa 897
Gly Lys Phe Lys Glu Leu Ile Glu Ser Thr Ser Lys Asp Ile Leu Lys
      230      235      240
gag ata ctt aca gat aat acc ggt aac ttt aaa ggc ctt ata gaa agc 945
Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly Leu Ile Glu Ser
      245      250      255
act ggc aag gag aaa gta aaa gaa ctt ctt atc gat ggg aag ttt aag 993
Thr Gly Lys Glu Lys Val Lys Glu Leu Leu Ile Asp Gly Lys Phe Lys
      260      265      270
gac ctg ttt act gat gca aca aaa gcc ggt tal gta aaa gau ata ctcl041
Asp Leu Phe Thr Asp Ala Thr Lys Ala Gly Tyr Val Lys Glu Ile Leu
      275      280      285
acg aac gal aca gct aag gaa gta ctt aca gat caa aca gca aag gagl089
Thr Asn Asp Thr Ala Lys Glu Val Leu Thr Asp Gln Thr Ala Lys Glu
      290      295      300      305
gtc cta aaa gat agt aca gct uua qac ata tta aag gac aca aac gcall37
Val Leu Lys Asp Ser Thr Ala Lys Asp Ile Leu Lys Asp Thr Asn Ala
      310      315      320
gct gcg gta cta aaa aac agc aca gct aaa gaa ata ctt aca aac caal185
Ala Ala Val Leu Lys Asn Ser Thr Ala Lys Glu Ile Leu Thr Asn Gln
      325      330      335
acc gct uua gaa gtg ctt aca gat ggt aca tcc aaa gaa gta cta aal233
Thr Ala Lys Glu Val Leu Thr Asp Gly Thr Ser Lys Glu Val Leu Lys
      340      345      350
gag ata ctt act tqt gat aaa ttt aaa gag gca gta aca gga gat ggtl281
Glu Ile Leu Thr Cys Asp Lys Phe Lys Glu Ala Val Thr Gly Asp Gly
      355      360      365
aaa gac ala cta aaa ggt ata ctt aca gat agc act ggt aag ttt aal329
Lys Asp Ile Leu Lys Gly Ile Leu Thr Asp Ser Thr Gly Lys Phe Lys
      370      375      380      385
gaa ctt atu gaa agt act ggt aaa qac ata ctg aaa qac att ctt aal377
Glu Leu Ile Glu Ser Thr Gly Lys Asp Ile Leu Lys Asp Ile Leu Thr

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          390          395          400
gat aqc act ggt aaa ttt uua gaa ctt ata gaa gta ctg gta aag aac1425
Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Glu Val Leu Val Lys Asn
          405          410          415
aag cta aaa gag att ctt aca gat aac acc ggt aac ttc uua ggg ctt1473
Lys Leu Lys Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly Leu
          420          425          430
gta gaa ggc gcc ggg aag gat gaa gca aaa gca gta ctt act gac gag1521
Val Glu Gly Ala Gly Lys Asp Glu Ala Lys Ala Val Leu Thr Asp Glu
          435          440          445
aaa ttt aaa ggc ttg ttt gat gac aaa aca ata gct ggc tat gta aau1569
Lys Phe Lys Gly Leu Phe Asp Asp Lys Thr Ile Ala Gly Tyr Val Lys
          450          455          460          465
gaa ata ctc acc agc gag aag ttt aaa aca ctg ttt gaa agl gca ggt1617
Glu Ile Leu Thr Ser Glu Lys Phe Lys Lys Leu Phe Glu Ser Ala Gly
          470          475          480          485
aag act aaa gta aaa gaa ctc ctc att gal gag aag ttt caa aaa tta1665
Lys Thr Lys Val Lys Glu Leu Leu Ile Asp Glu Lys Phe Gln Lys Leu
          485          490          495
ttt gag gat gac acg aaa gcc agt cal gta uua gaa ata ctc acg aac1713
Phe Glu Asp Asp Thr Lys Ala Ser His Val Lys Gln Ile Leu Thr Asn
          500          505          510
gut aca gct aag gaa ala ctt aca gat caa aca gct aau gaa gtc cta1761
Asp Thr Ala Lys Glu Ile Leu Thr Asp Gln Thr Ala Lys Glu Val Leu
          515          520          525
aag gat agt acu gct aaa gag ata tta aag gac aca aac gca gct gcg1809
Lys Asp Ser Thr Ala Lys Glu Ile Leu Lys Asp Thr Asn Ala Ala Ala
          530          535          540          545
cta cta aaa gac agc aca gca aaa gag gta cta aaa tcc gat aaa ttt1857
Leu Leu Lys Asp Ser Thr Ala Lys Glu Val Leu Lys Ser Asp Lys Phe
          550          555          560
aaa gat gca ata act ggt gct ggl aag gac gca cta aaa gag ata ctt1905
Lys Asp Ala Ile Thr Gly Ala Gly Lys Asp Ala Leu Lys Glu Ile Leu
          565          570          575
act tgt gat aaa ttt aaa gag gca gta aca ggc aat ggt aau gac ata1953
Thr Cys Asp Lys Phe Lys Glu Ala Val Thr Gly Asn Gly Lys Asp Ile
          580          585          590
cta aau ggt ata ctt aca gat agc act ggt aaa ttt aaa gag cta ata2001
Leu Lys Gly Ile Leu Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile
          595          600          605
gaa agc act ggt aag gat aag cta aau gag att ctt aca gat aac acc2049
Glu Ser Thr Gly Lys Asp Lys Leu Lys Glu Ile Leu Thr Asp Asn Thr
          610          615          620          625
ggt aac ttt uua ttt ctt gta gaa gcc gcc ggt aag gat gaa gca aaa2097
Gly Asn Phe Lys Phe Leu Val Glu Gly Ala Gly Lys Asp Glu Ala Lys
          630          635          640
gca gta ctt act cac gag aaa ttt aaa gac ttg ttt aat gtc aaa aca2145
Ala Val Leu Thr His Glu Lys Phe Lys Asp Leu Phe Asn Val Lys Thr
          645          650          655
aca gct ggc tac gtg aaa gaa ata ctt acc agc gac aag ttt aaa gaa2193
Thr Ala Gly Tyr Val Lys Glu Ile Leu Thr Ser Asp Lys Phe Lys Glu
          660          665          670
ctg ttt act gat gca aca aaa gct ggc tac gtg uua gaa ata ctc acg2241
Leu Phe Thr Asp Ala Thr Lys Ala Gly Tyr Val Lys Glu Ile Leu Thr
          675          680          685
aac gat aca gct aag gaa ata ctt aca gat caa aca gct aaa gaa gtc2289
Asn Asp Thr Ala Lys Glu Ile Leu Thr Asp Gln Thr Ala Lys Gln Val

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690          695          700          705
cta aag gat ggt aca gct aaa gac ata tta aag gac aca aac gca cgt2337
Leu Lys Asp Gly Thr Ala Lys Asp Ile Leu Lys Asp Thr Asn Ala Arg
          710          715          720
gcg cta cta aaa gac agc aca gcc aaa gaa gta cta aaa tgc gat aaa2385
Ala Leu Leu Lys Asp Ser Thr Ala Lys Glu Val Leu Lys Cys Asp Lys
          725          730          735
ttt aag gaa gca ata aca ggt gcc ggt aaa gat gag cta aaa tac ata2433
Phe Lys Glu Ala Ile Thr Gly Ala Gly Lys Asp Glu Leu Lys Tyr Ile
          740          745          750
ctc act aat agc gag ttt aaa agc tta ttt cat agc aaa gat agc gct2481
Leu Thr Asn Ser Glu Phe Lys Ser Leu Phe His Ser Lys Asp Ser Ala
          755          760          765
gaa gct gtt aaa gca ala ttt acc cac aat aag ttt aaa gaa cta ctt2529
Glu Ala Val Lys Ala Ile Phe Thr His Asn Lys Phe Lys Glu Leu Leu
          770          775          780          785
gaa cat gca aga aca acc cua aca ata cgc aag cgc ttt gca aat gct2577
Glu His Ala Arg Thr Thr Gln Thr Ile Arg Arg Arg Phe Ala Asn Ala
          790          795          800
tta gat caa cta aaa gcg cta att acc tgt ggc aac ggt gat cat gca2625
Leu Asp Gln Leu Lys Ala Leu Ile Thr Cys Gly Ser Gly Asp His Ala
          805          810          815
aca aaa cta caa gcc ttt gga agt gca cta tgc acc aaa aag aag gag2673
Thr Lys Leu Gln Ala Phe Gly Ser Ala Leu Cys Thr Lys Lys Lys Glu
          820          825          830
ttg tgc agt aat ttt agc tgt gca aac tgc agt agt acu aca act gaa2721
Leu Cys Ser Asn Phe Ser Cys Ala Asn Cys Ser Ser Thr Thr Thr Ala
          835          840          845
taattacgta gcgctaggtg ggggtaattt accccacct agctaqaatc acacgggggaa 2781
ctttctctct attactaggg tcttaggatt tacaacaaaa ttactatgac agcca 2836

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<200> SEQUENCE CHARACTERISTICS:

<210> SEQ ID NO 4

<211> LENGTH: 849

<212> TYPE: PRT

<213> ORGANISM: Ehrlichia risticii

<400> SEQUENCE: 4

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  1          5          10          15
Ala Asn Leu Val Asp Glu Leu Leu Leu Ile Leu Val Lys Asp Ser Ile
  20          25          30
Phe Thr Gln Val Ile Lys Gly Glu Gly Lys Thr Glu Leu Lys Asp Ile
  35          40          45
Leu Thr Asp Asn Thr Gly Lys Phe Lys Glu Leu Ile Glu Ser Ala Gly
  50          55          60
Lys Asp Ile Leu Lys Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys
  65          70          75          80
Gly Leu Ile Glu Gly Asn Gly Lys Thr Glu Ala Lys Glu Val Arg Thr
  85          90          95
Asn Glu Lys Phe Lys Glu Leu Phe Gly Ser Asn Gly Lys Asp Ile Leu
  100          105          110
Lys Asp Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly Leu Ile Glu
  115          120          125
Ser Ala Ala Lys Gly Lys Leu Lys Asp Leu Leu Ile Asp Glu Lys Phe
  130          135          140
Gln Lys Leu Phe Glu Asp Glu Thr Lys Ala Gly Arg Val Lys Glu Ile
  145          150          155          160

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Leu Thr Asp Ser Asn Ala Lys Glu Ile Leu Thr Asn Glu Val Ala Lys
 165 170 175
 Glu Val Leu Lys Ser Asp Lys Phe Lys Glu Ala Ile Thr Gly Asp Gly
 180 185 190
 Lys Asp Ala Leu Lys Glu Ile Leu Thr Cys Asp Lys Phe Lys Glu Ala
 195 200 205
 Val Thr Gly Asn Gly Lys Asp Ile Leu Lys Gly Ile Leu Thr Asp Ser
 210 215 220
 Thr Gly Lys Phe Lys Glu Leu Ile Glu Ser Thr Ser Lys Asp Ile Leu
 225 230 235 240
 Lys Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly Leu Ile Glu
 245 250 255
 Ser Thr Gly Lys Glu Lys Val Lys Glu Leu Leu Ile Asp Gly Lys Phe
 260 265 270
 Lys Asp Leu Phe Thr Asp Ala Thr Lys Ala Gly Tyr Val Lys Glu Ile
 275 280 285
 Leu Thr Asn Asp Thr Ala Lys Glu Val Leu Thr Asp Glu Thr Ala Lys
 290 295 300
 Glu Val Leu Lys Asp Ser Thr Ala Lys Asp Ile Leu Lys Asp Thr Asn
 305 310 315 320
 Ala Ala Ala Val Leu Lys Asn Ser Thr Ala Lys Glu Ile Leu Thr Asn
 325 330 335
 Glu Thr Ala Lys Glu Val Leu Thr Asp Gly Thr Ser Lys Glu Val Leu
 340 345 350
 Lys Glu Ile Leu Thr Cys Asp Lys Phe Lys Glu Ala Val Thr Gly Asp
 355 360 365
 Gly Lys Asp Ile Leu Lys Gly Ile Leu Thr Asp Ser Thr Gly Lys Phe
 370 375 380
 Lys Glu Leu Ile Glu Ser Thr Gly Lys Asp Ile Leu Lys Asp Ile Leu
 385 390 395 400
 Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Glu Val Leu Val Lys
 405 410 415
 Asn Lys Leu Lys Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly
 420 425 430
 Leu Val Glu Gly Ala Gly Lys Asp Glu Ala Lys Ala Val Leu Thr Asp
 435 440 445
 Glu Lys Phe Lys Gly Leu Phe Asp Asp Lys Thr Ile Ala Gly Tyr Val
 450 455 460
 Lys Glu Ile Leu Thr Ser Glu Lys Phe Lys Lys Leu Phe Glu Ser Ala
 465 470 475 480
 Gly Lys Thr Lys Val Lys Glu Leu Leu Ile Asp Glu Lys Phe Glu Lys
 485 490 495
 Leu Phe Glu Asp Thr Lys Ala Ser His Val Lys Glu Ile Leu Thr
 500 505 510
 Asn Asp Thr Ala Lys Glu Ile Leu Thr Asp Glu Thr Ala Lys Glu Val
 515 520 525
 Leu Lys Asp Ser Thr Ala Lys Glu Ile Leu Lys Asp Thr Asn Ala Ala
 530 535 540
 Ala Leu Leu Lys Asp Ser Thr Ala Lys Glu Val Leu Lys Ser Asp Lys
 545 550 555 560
 Phe Lys Asp Ala Ile Thr Gly Ala Gly Lys Asp Ala Leu Lys Glu Ile
 565 570 575
 Leu Thr Cys Asp Lys Phe Lys Glu Ala Val Thr Gly Asn Gly Lys Asp
 580 585 590
 Ile Leu Lys Gly Ile Leu Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu
 595 600 605
 Ile Glu Ser Thr Gly Lys Asp Lys Leu Lys Glu Ile Leu Thr Asp Asn

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        610                615                620
Thr Gly Asn Phe Lys Phe Leu Val Glu Gly Ala Gly Lys Asp Glu Ala
625                630                635                640
Lys Ala Val Leu Thr His Glu Lys Phe Lys Asp Leu Phe Asn Val Lys
        645                650                655
Thr Thr Ala Gly Tyr Val Lys Glu Ile Leu Thr Ser Asp Lys Phe Lys
        660                665                670
Glu Leu Phe Thr Asp Ala Thr Lys Ala Gly Tyr Val Lys Glu Ile Leu
        675                680                685
Thr Asn Asp Thr Ala Lys Glu Ile Leu Thr Asp Gln Thr Ala Lys Glu
690                695                700
Val Leu Lys Asp Gly Thr Ala Lys Asp Ile Leu Lys Asp Thr Asn Ala
705                710                715                720
Arg Ala Leu Leu Lys Asp Ser Thr Ala Lys Glu Val Leu Lys Cys Asp
        725                730                735
Lys Phe Lys Glu Ala Ile Thr Gly Ala Gly Lys Asp Glu Leu Lys Tyr
        740                745                750
Ile Leu Thr Asn Ser Glu Phe Lys Ser Leu Phe His Ser Lys Asp Ser
        755                760                765
Ala Glu Ala Val Lys Ala Ile Phe Thr His Asn Lys Phe Lys Glu Leu
770                775                780
Leu Glu His Ala Arg Thr Gln Thr Ile Arg Arg Arg Phe Ala Asn
785                790                795                800
Ala Leu Asp Gln Leu Lys Ala Leu Ile Thr Cys Gly Ser Gly Asp His
        805                810                815
Ala Thr Lys Leu Gln Ala Phe Gly Ser Ala Leu Cys Thr Lys Lys Lys
        820                825                830
Glu Leu Cys Ser Asn Phe Ser Cys Ala Asn Cys Ser Ser Thr Thr Thr
        835                840                845
Ala

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<200> SEQUENCE CHARACTERISTICS:

<210> SEQ ID NO 5

<211> LENGTH: 1937

<212> TYPE: DNA

<213> ORGANISM: Ehrlichia risticii

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (175)..(1791)

<400> SEQUENCE: 5

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tttataacua aggactaccc tccctacata aaalattctaa gacgaaaaat ccoct atg 177
Met
1
tca aat gaa aca ctt ctg agc gla ctt tct gat gaa acg cac ttt gcl225
Ser Asn Glu Thr Leu Leu Ser Val Leu Ser Asp Glu Thr His Phe Ala
5 10 15
aat cta gtt gat gaa ctt ctt ctc agc ttc gtt aaa gac agt att ttc273
Asn Leu Val Asp Glu Leu Leu Leu Ser Leu Val Lys Asp Ser Ile Phe
20 25 30
act caa gta ata aaa ggc gag gga aag ucu gaa tta aaa gac att ctt321
Thr Gln Val Ile Lys Gly Glu Gly Lys Thr Glu Leu Lys Asp Ile Leu
35 40 45
aca gat agc act ggc aag ttt aaa gag ctg ata gga agt agc ggt aag369
Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Gly Ser Ser Gly Lys
50 55 60 65

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gat ata cta aaa agc ata cac aca gat ggc tca ggc aac ttt aaa ggc417
Asp Ile Leu Lys Ser Ile His Thr Asp Gly Ser Gly Asn Phe Lys Gly
70 75 80
ctt ata caa agc aca ggt aag gca gaa aaa gag gta ctc act aat465
Leu Ile Gln Ser Thr Gly Lys Ala Glu Val Lys Glu Val Leu Thr Asn
85 90 95
gaa aaa ttc aaa gag ctt ttt gga agc gaa ggt aaa gac ata cta aaa513
Glu Lys Phe Lys Glu Leu Phe Gly Ser Glu Gly Lys Asp Ile Leu Lys
100 105 110
gag ata ctt aca gac aat acc ggc aat ttt aaa ggc ctt ala gaa ggc561
Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly Leu Ile Glu Gly
115 120 125
aaa ggt aag gat gaa gca aaq gga gta ctt act gac gag aaa ttt aaa609
Lys Gly Lys Asp Glu Ala Lys Gly Val Leu Thr Asp Glu Lys Phe Lys
130 135 140 145
ggc ttg ttt gat gac aaa acu ata gct ggc tat gta aaa gaa ata ctc657
Gly Leu Phe Asp Asp Lys Thr Ile Ala Gly Tyr Val Lys Glu Ile Leu
150 155 160
acc agc gag agt tta aua aac tgt ttg aaa ggt gca ggt aag uct aaa705
Thr Ser Glu Ser Leu Lys Asn Cys Leu Lys Gly Ala Gly Lys Thr Lys
165 170 175
gta aua gaa ctc ctc att gat gag aag ttt caa aaa tta ttt gag gat753
Val Lys Glu Leu Leu Ile Asp Glu Lys Phe Gln Lys Leu Phe Glu Asp
180 185 190
gac acg aaa gcc agt cat gta aua gaa ata ctt aca gac agt aac gct801
Asp Thr Lys Ala Ser His Val Lys Glu Ile Leu Thr Asp Ser Asn Ala
195 200 205
aag gaa ata ctc aca aat gaa gta gca aaa gag gta cta aaa tcc gat849
Lys Glu Ile Leu Thr Asn Glu Val Ala Lys Glu Val Leu Lys Ser Asp
210 215 220 225
aaa ttt aaa gal gca ata act ggt gct ggt aaq gac gca cta aaa gag897
Lys Phe Lys Asp Ala Ile Thr Gly Ala Gly Lys Asp Ala Leu Lys Glu
230 235 240
ata ctt act tgc gat aaa ttt aaa gat gca gta aca ggt aat ggt aag945
Ile Leu Thr Cys Asp Lys Phe Lys Asp Ala Val Thr Gly Asn Gly Lys
245 250 255
gac gca cta aua gaa ata ctt act tgc gat aaa ttt aaa gat gca gta993
Asp Ala Leu Lys Glu Ile Leu Thr Cys Asp Lys Phe Lys Asp Ala Val
260 265 270
acu ggc aat ggt aaa gac aag cta aaa gag att ctt act ctc gag aag1041
Thr Gly Asn Gly Lys Asp Lys Leu Lys Glu Ile Leu Thr His Glu Lys
275 280 285
ttt aaa gca ctc ala gag agt gaa ggc aaa gac ata ctg aaa gaa att1089
Phe Lys Ala Leu Ile Glu Ser Glu Gly Lys Asp Ile Leu Lys Glu Ile
290 295 300 305
ctt aca gat agt acc ggt aaa ttt aaa gag cta ata gaa agc act ggt1137
Leu Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Glu Ser Thr Gly
310 315 320
aaa gac aag cta aaa gag att ttc aca gal aac acc ggt aac ttt aaal185
Lys Asp Lys Leu Lys Glu Ile Phe Thr Asp Asn Thr Gly Asn Phe Lys
325 330 335
ggg ctt gta gaa ggc gcc ggt aag gat gaa gca aaa gca gta ctt act1233
Gly Leu Val Glu Gly Ala Gly Lys Asp Glu Ala Lys Ala Val Leu Thr
340 345 350
cac gag aaa ttt aaa gac ttg ttt aat gac aaa aca aca gcl ggc tac1281
His Glu Lys Phe Lys Asp Leu Phe Asn Asp Lys Thr Thr Ala Gly Tyr
355 360 365

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gtg aaa gaa ata ctc acc agt gat aag ttt aaa aaa tta ttt gag gac1329
Val Lys Glu Ile Leu Thr Ser Asp Lys Phe Lys Lys Leu Phe Glu Asp
370 375 380 385
aat acc aaa gct qgc tac gtg aaa gaa ata ctc ucg aac gat aca gct1377
Asn Thr Lys Ala Gly Tyr Val Lys Glu Ile Leu Thr Asn Asp Thr Ala
390 395 400
aag gaa atu ctc aca aat caa aca gct aaa gaa gtc cta aaa gac agc1425
Lys Glu Ile Leu Thr Asn Gln Thr Ala Lys Glu Val Leu Lys Asp Ser
405 410 415
aca gcc aaa gaa ata cta aaa tgc gat aaa ttt aag gac gca ata aca1473
Thr Ala Lys Glu Ile Leu Lys Cys Asp Lys Phe Lys Asp Ala Ile Thr
420 425 430
ggc gct ggt aaa gat gac cta aaa tac ata ctc act aat aac gag ttt1521
Gly Ala Gly Lys Asp Glu Leu Lys Tyr Ile Leu Thr Asn Asn Glu Phe
435 440 445
aaa agc tta ttt gat agc aaa gat agc gct gaa gct gtt aaa gca ata1569
Lys Ser Leu Phe Asp Ser Lys Asp Ser Ala Glu Ala Val Lys Ala Ile
450 455 460 465
ttt acc cac aat aag ttt aaa gaa cta ctt aaa acg lgc aag gac aac1617
Phe Thr His Asn Lys Phe Lys Glu Leu Leu Lys Thr Cys Lys Asp Asn
470 475 480
cca aaa aat acg gcg gcg ctt gca gct gct tta gat gaa cta aaa gal1665
Pro Lys Asn Thr Ala Ala Leu Ala Ala Leu Asp Glu Leu Lys Asp
485 490 495
cta att acg tgt gac cgc aat aat cat gca aca aaa cta caa gcc ttt1713
Leu Ile Thr Cys Asp Arg Asn Asn His Ala Thr Lys Leu Gln Ala Phe
500 505 510
gga agt gca cta tgc acc aga aau uau gag tcg tgc gat aat ttt agc1761
Gly Ser Ala Leu Cys Thr Arg Lys Lys Glu Ser Cys Asp Asn Phe Ser
515 520 525
cct gca agc tgc agt agt aca gca gct aca taattacgta gcgctaggtg 1811
Pro Ala Ser Cys Ser Ser Thr Ala Ala Thr
530 535
ggggtaaatt aacccacact acgtagaatc acacggggaa cttctctctt attactgagg 1871
tcttaggatt tacttlcaaa ttactatguc agccgattaa attattatga cagacgatac 1931
actttt 1937

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<200> SEQUENCE CHARACTERISTICS:

<210> SEQ ID NO 6

<211> LENGTH: 539

<212> TYPE: PRT

<213> ORGANISM: Ehrlichia risticii

<400> SEQUENCE: 6

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Met Ser Asn Glu Thr Leu Leu Ser Val Leu Ser Asp Glu Thr His Phe
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Ala Asn Leu Val Asp Glu Leu Leu Leu Ser Leu Val Lys Asp Ser Ile
20 25 30
Phe Thr Gln Val Ile Lys Gly Glu Gly Lys Thr Glu Leu Lys Asp Ile
35 40 45
Leu Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Gly Ser Ser Gly
50 55 60
Lys Asp Ile Leu Lys Ser Ile His Thr Asp Gly Ser Gly Asn Phe Lys
65 70 75 80
Gly Leu Ile Gln Ser Thr Gly Lys Ala Glu Val Lys Glu Val Leu Thr
85 90 95
Asn Glu Lys Phe Lys Glu Leu Phe Gly Ser Glu Gly Lys Asp Ile Leu
100 105 110

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Lys Glu Ile Leu Thr Asp Asn Thr Gly Asn Phe Lys Gly Leu Ile Glu
    115                      120                      125
Gly Lys Gly Lys Asp Glu Ala Lys Gly Val Leu Thr Asp Glu Lys Phe
    130                      135                      140
Lys Gly Leu Phe Asp Asp Lys Thr Ile Ala Gly Tyr Val Lys Glu Ile
    145                      150                      155                      160
Leu Thr Ser Glu Ser Leu Lys Asn Cys Leu Lys Gly Ala Gly Lys Thr
    165                      170                      175
Lys Val Lys Glu Leu Leu Ile Asp Glu Lys Phe Gln Lys Leu Phe Glu
    180                      185                      190
Asp Asp Thr Lys Ala Ser His Val Lys Glu Ile Leu Thr Asp Ser Asn
    195                      200                      205
Ala Lys Glu Ile Leu Thr Asn Glu Val Ala Lys Glu Val Leu Lys Ser
    210                      215                      220
Asp Lys Phe Lys Asp Ala Ile Thr Gly Ala Gly Lys Asp Ala Leu Lys
    225                      230                      235                      240
Glu Ile Leu Thr Cys Asp Lys Phe Lys Asp Ala Val Thr Gly Asn Gly
    245                      250                      255
Lys Asp Ala Leu Lys Glu Ile Leu Thr Cys Asp Lys Phe Lys Asp Ala
    260                      265                      270
Val Thr Gly Asn Gly Lys Asp Lys Leu Lys Glu Ile Leu Thr His Glu
    275                      280                      285
Lys Phe Lys Ala Leu Ile Glu Ser Glu Gly Lys Asp Ile Leu Lys Glu
    290                      295                      300
Ile Leu Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Glu Ser Thr
    305                      310                      315                      320
Gly Lys Asp Lys Leu Lys Glu Ile Phe Thr Asp Asn Thr Gly Asn Phe
    325                      330                      335
Lys Gly Leu Val Glu Gly Ala Gly Lys Asp Glu Ala Lys Ala Val Leu
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Thr His Glu Lys Phe Lys Asp Leu Phe Asn Asp Lys Thr Thr Ala Gly
    355                      360                      365
Tyr Val Lys Glu Ile Leu Thr Ser Asp Lys Phe Lys Lys Leu Phe Glu
    370                      375                      380
Asp Asn Thr Lys Ala Gly Tyr Val Lys Glu Ile Leu Thr Asn Asp Thr
    385                      390                      395                      400
Ala Lys Glu Ile Leu Thr Asn Gln Thr Ala Lys Glu Val Leu Lys Asp
    405                      410                      415
Ser Thr Ala Lys Glu Ile Leu Lys Cys Asp Lys Phe Lys Asp Ala Ile
    420                      425                      430
Thr Gly Ala Gly Lys Asp Glu Leu Lys Tyr Ile Leu Thr Asn Asn Glu
    435                      440                      445
Phe Lys Ser Leu Phe Asp Ser Lys Asp Ser Ala Glu Ala Val Lys Ala
    450                      455                      460
Ile Phe Thr His Asn Lys Phe Lys Glu Leu Leu Lys Thr Cys Lys Asp
    465                      470                      475                      480
Asn Pro Lys Asn Thr Ala Ala Leu Ala Ala Leu Asp Glu Leu Lys
    485                      490                      495
Asp Leu Ile Thr Cys Asp Arg Asn Asn His Ala Thr Lys Leu Gln Ala
    500                      505                      510
Phe Gly Ser Ala Leu Cys Thr Arg Lys Lys Glu Ser Cys Asp Asn Phe
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<213> ORGANISM: Ehrlichia risticii

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 ttcataacaa aggactalcc tccttgcata aaattttctaa gacgaaaaat cctt atg 177

Met

1

toa aat gaa aca ctt ctg agc gta ctt let gat gaa acg cac ttt gct 225
 Ser Asn Glu Thr Leu Leu Ser Val Leu Ser Asp Glu Thr His Phe Ala
 5 10 15
 aat cta gtt gat gaa ctt ctt ctc agc ttg qtt aaa gac agt att ttc 273
 Asn Leu Val Asp Glu Leu Leu Leu Ser Leu Val Lys Asp Ser Ile Phe
 20 25 30
 act caa gta ata aau ggc gag gga aag aca gaa lta aau gac att ctt 321
 Thr Gln Val Ile Lys Gly Glu Gly Lys Thr Glu Leu Lys Asp Ile Leu
 35 40 45
 aca gat agc act ggc aag ttt aaa gag ctg ata gga agt agc ggt aag 369
 Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Gly Ser Ser Gly Lys
 50 55 60 65
 gat ata ctu aaa agc ata ctc aca gat ggc tca ggc aac ttt aaa ggc 417
 Asp Ile Leu Lys Ser Ile Leu Thr Asp Gly Ser Gly Asn Phe Lys Gly
 70 75 80
 ctt ata caa agc aca ggt aag gca gaa gta aaa qag gta ctc act aat 465
 Leu Ile Gln Ser Thr Gly Lys Ala Glu Val Lys Glu Val Leu Thr Asn
 85 90 95
 gaa aau ttc aaa gag ctt ttt qga agc gal ggt aag gat ata tta aaa 513
 Glu Lys Phe Lys Glu Leu Phe Gly Ser Asp Gly Lys Asp Ile Leu Lys
 100 105 110
 gac ata ctc aca gal agc act ggt aag ttt aaa gag ctg ata gga agt 561
 Asp Ile Leu Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Gly Ser
 115 120 125
 agc ggt aag gac ata cta aaa aac att ctt uca gat agc acc ggt aag 609
 Ser Gly Lys Asp Ile Leu Lys Asn Ile Leu Thr Asp Ser Thr Gly Lys
 130 135 140 145
 ttt aaa gaa ctt ata gaa agt gca ggt aag ggt aag ctg aaa gac ctt 657
 Phe Lys Glu Leu Ile Glu Ser Ala Gly Lys Gly Lys Leu Lys Asp Leu
 150 155 160
 ctt att gat gga aac ttt aaa aaa tta ttt gag gal gac acg aaa gct 705
 Leu Ile Asp Gly Asn Phe Lys Lys Leu Phe Glu Asp Asp Thr Lys Ala
 165 170 175
 gct cat gta aaa gaa ata ctt aca gac agc aac gct aag gaa ata ctc 753
 Ala His Val Lys Glu Ile Leu Thr Asp Ser Asn Ala Lys Glu Ile Leu
 180 185 190
 aca aat gaa gta gca aaa gag gta cta aaa tcc gat aaa ttt aaa gat 801
 Thr Asn Glu Val Ala Lys Glu Val Leu Lys Ser Asp Lys Phe Lys Asp
 195 200 205
 gca ata act ggt ggt ggt aag gac gca cta aaa gag ata ctt act tgc 849
 Ala Ile Thr Gly Ala Gly Lys Asp Ala Leu Lys Glu Ile Leu Thr Cys
 210 215 220 225
 gat aaa ttt aaa gal gca gta aca ggc aat ggt aag gac gca cta aaa 897
 Asp Lys Phe Lys Asp Ala Val Thr Gly Asn Gly Lys Asp Ala Leu Lys
 230 235 240

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gaa ata ctt acL tgc gat aaa ttt aaa gat gca gta aca ggc aat ggt 945
Glu Ile Leu Thr Cys Asp Lys Phe Lys Asp Ala Val Thr Gly Asn Gly
245 250 255
aaa gac aaq cta aaa gag att ctt acL cac gag aag ttt aaa gca ctc 993
Lys Asp Lys Leu Lys Glu Ile Leu Thr His Glu Lys Phe Lys Ala Leu
260 265 270
ata gag agt gaa ggc aaa gac ala ctg aaa gac att ctt aca gat agt1041
Ile Glu Ser Glu Gly Lys Asp Ile Leu Lys Asp Ile Leu Thr Asp Ser
275 280 285
acc ggt aaa ttt aaa gag cta ata gaa agc acg ggt aag gat gaa gca1089
Thr Gly Lys Phe Lys Glu Leu Ile Glu Ser Thr Gly Lys Asp Glu Ala
290 295 300 305
aaa gca gta ctt act gac gag aaa ttt auu qac ttg ttt aat gac aaal137
Lys Ala Val Leu Thr Asp Glu Lys Phe Lys Asp Leu Phe Asn Asp Lys
310 315 320
aca aca gct ggc tac gtg aaa gaa ala ctc acc agt gat aag ttt aaal185
Thr Thr Ala Gly Tyr Val Lys Glu Ile Leu Thr Ser Asp Lys Phe Lys
325 330 335
aaa tta ttt gag gac aat acc aaa gct ggc tac gtg aaa gaa ata ctc1233
Lys Leu Phe Glu Asp Asn Thr Lys Ala Gly Tyr Val Lys Glu Ile Leu
340 345 350
acg aac gat aca gct aag gaa ata ctt acc aat cat aaa ttt aag gaal281
Thr Asn Asp Thr Ala Lys Glu Ile Leu Thr Asn His Lys Phe Lys Glu
355 360 365
gca ata uct ggc gat ggt aaa gac ata ctg aaa gaa att ctt aca gat1329
Ala Ile Thr Gly Asp Gly Lys Asp ile Leu Lys Glu Ile Leu Thr Asp
370 375 380 385
agc act ggt aac ttt aaa ggc gca ata aca ggt gcc ggt aaa gat caal377
Ser Thr Gly Asn Phe Lys Gly Ala ile Thr Gly Ala Gly Lys Asp Gln
390 395 400
cta aaa tac ata ctc acL aat agc gag ttt aaa agc tta ttt gat agc1425
Leu Lys Tyr Ile Leu Thr Asn Ser Glu Phe Lys Ser Leu Phe Asp Ser
405 410 415
aaa gat agc gct gaa gct gtt aaa gaa ata ttt acc cac agl aag ttt1473
Lys Asp Ser Ala Glu Ala Val Lys Glu Ile Phe Thr His Ser Lys Phe
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435 440 445
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Leu Ala Ala Ala Leu Asp Glu Leu Lys Asp Leu Ile Thr Cys Gly Ser
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Gly Asp His Ala Thr Lys Leu Gln Ala Phe Gly Ser Ala Leu Cys Thr
470 475 480
aga aaa aaa gag tgc tgc gat aal LLE agc tct gca aac tgc agt agt1665
Arg Lys Lys Glu Ser Cys Asp Asn Phe Ser Ser Ala Asn Cys Ser Ser
485 490 495
aca aca act gca taattacgta qcgctagggtg ggggtAattt acccccacct 1717
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<211> LENGTH: 501

<212> TYPE: PRT

<213> ORGANISM: Ehrlichia risticii

<400> SEQUENCE: 8

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 20           25           30
Phe Thr Gln Val Ile Lys Gly Glu Gly Lys Thr Glu Leu Lys Asp Ile
 35           40           45
Leu Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Gly Ser Ser Gly
 50           55           60
Lys Asp Ile Leu Lys Ser Ile Leu Thr Asp Gly Ser Gly Asn Phe Lys
 65           70           75           80
Gly Leu Ile Gln Ser Thr Gly Lys Ala Glu Val Lys Glu Val Leu Thr
 85           90           95
Asn Glu Lys Phe Lys Glu Leu Phe Gly Ser Asp Gly Lys Asp Ile Leu
100          105          110
Lys Asp Ile Leu Thr Asp Ser Thr Gly Lys Phe Lys Glu Leu Ile Gly
115          120          125
Ser Ser Gly Lys Asp Ile Leu Lys Asn Ile Leu Thr Asp Ser Thr Gly
130          135          140
Lys Phe Lys Glu Leu Ile Glu Ser Ala Gly Lys Gly Lys Leu Lys Asp
145          150          155          160
Leu Leu Ile Asp Gly Asn Phe Lys Lys Leu Phe Glu Asp Asp Thr Lys
165          170          175
Ala Ala His Val Lys Glu Ile Leu Thr Asp Ser Asn Ala Lys Glu Ile
180          185          190
Leu Thr Asn Glu Val Ala Lys Glu Val Leu Lys Ser Asp Lys Phe Lys
195          200          205
Asp Ala Ile Thr Gly Ala Gly Lys Asp Ala Leu Lys Glu Ile Leu Thr
210          215          220
Cys Asp Lys Phe Lys Asp Ala Val Thr Gly Asn Gly Lys Asp Ala Leu
225          230          235          240
Lys Glu Ile Leu Thr Cys Asp Lys Phe Lys Asp Ala Val Thr Gly Asn
245          250          255
Gly Lys Asp Lys Leu Lys Glu Ile Leu Thr His Glu Lys Phe Lys Ala
260          265          270
Leu Ile Glu Ser Glu Gly Lys Asp Ile Leu Lys Asp Ile Leu Thr Asp
275          280          285
Ser Thr Gly Lys Phe Lys Glu Leu Ile Glu Ser Thr Gly Lys Asp Glu
290          295          300
Ala Lys Ala Val Leu Thr Asp Glu Lys Phe Lys Asp Leu Phe Asn Asp
305          310          315          320
Lys Thr Thr Ala Gly Tyr Val Lys Glu Ile Leu Thr Ser Asp Lys Phe
325          330          335
Lys Lys Leu Phe Glu Asp Asn Thr Lys Ala Gly Tyr Val Lys Glu Ile
340          345          350
Leu Thr Asn Asp Thr Ala Lys Glu Ile Leu Thr Asn His Lys Phe Lys
355          360          365
Glu Ala Ile Thr Gly Asp Gly Lys Asp Ile Leu Lys Glu Ile Leu Thr
370          375          380
Asp Ser Thr Gly Asn Phe Lys Gly Ala Ile Thr Gly Ala Gly Lys Asp
385          390          395          400
Gln Leu Lys Tyr Ile Leu Thr Asn Ser Glu Phe Lys Ser Leu Phe Asp
405          410          415
Ser Lys Asp Ser Ala Glu Ala Val Lys Glu Ile Phe Thr His Ser Lys
420          425          430

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Phe Lys Glu Leu Leu Lys Thr Cys Lys Asp Asn Pro Lys Asn Thr Ala
      435              440              445
Ala Leu Ala Ala Ala Leu Asp Glu Leu Lys Asp Leu Ile Thr Cys Gly
      450              455              460
Ser Gly Asp His Ala Thr Lys Leu Gln Ala Phe Gly Ser Ala Leu Cys
      465              470              475              480
Thr Arg Lys Lys Glu Ser Cys Asp Asn Phe Ser Ser Ala Asn Cys Ser
      485              490              495
Ser Thr Thr Thr Ala
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<223> OTHER INFORMATION: Description of Artificial Sequence primer

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<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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33

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18

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18

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<400> SEQUENCE: 26
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11

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11

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11

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11

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<200> SEQUENCE CHARACTERISTICS:
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<213> ORGANISM: Ehrlichia risticii
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<200> SEQUENCE CHARACTERISTICS:
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<213> ORGANISM: Ehrlichia risticii
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<400> SEQUENCE: 40
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<211> LENGTH: 11
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<400> SEQUENCE: 41
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atggtaagga c 11

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acttatagaa g

11

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